In the Claims

1-21 (canceled)

22 (new). A method for producing a biochip including a support on which is immobilized a set of polynucleotides, which method comprises the steps of:

(i) obtaining BAC clones including a nucleic insert corresponding to or specific to a portion of a human genome,

(ii) selecting, from the BAC clones thus obtained, a set of BAC clones including a single nucleic insert in the human genome, the BAC clones of the selected set including nucleic inserts substantially uniformly distributed over the human genome, the selection step comprising:

(a) eliminating non-single clones;

(b) eliminating clones sharing a same STS;

(c) eliminating STS which are marked at least two different places on the human genome;

(d) classifying clones as a function of their position on the genome to defining neighbouring clones; and

(e) eliminating clones by applying an iterative method so as to obtain in particular substantially uniform distribution of the finally selected clones over the human genome; and

(iii) depositing, on a support, the selected clones or the nucleic inserts contained in said clones, or part of them, under conditions enabling the deposited clones or inserts to hybridise with a nucleic acid having a complementary sequence.

23 (new). The method according to claim 22, wherein step (i) comprises obtaining a collection of BAC clones including nucleic inserts likely to cover the whole sequence of the human genome.

24 (new). The method according to claim 22, wherein the BAC clones of the selected set include nucleic inserts spaced apart from one another by an interval of about 1Mb.

25 (new). The method according to claim 22, wherein selection steps a) to e), or part of them, are repeated at least once until a set of BAC clones is obtained including a single insert in the human genome, the BAC clones of the selected set furthermore including nucleic inserts substantially uniformly distributed over the human genome, and covering the whole human genome.

26 (new). The method according to claim 22, wherein step a) comprises compilation or analysis of the information known for a clone by computer analysis of the sequence of the nucleic insert contained therein and/or by biological experiments.

27 (new). The method according to claim 22, wherein step e) comprises a first sub-step (e_1) of extracting a sub-set of BAC clones likely to be eliminated from the finally selected set of clones, and a second sub-step (e_2), during which a second criterion is applied to the elements of the sub-set of clones likely to be eliminated, so as to determine the single clone of this sub-set which will be effectively eliminated.

28 (new). The method according to claim 27, wherein the first sub-step (e_1) of extracting from the sub-set BAC clones likely to be eliminated comprises applying a first rejection criterion that comprises defining a maximum authorized distance between two neighbouring clones of the finally selected set of clones.

29 (new). The method according to claim 27, wherein the second criterion applied during the second sub-step (e_2) includes requiring a minimum distance between two neighbouring clones of the finally selected set of clones.

30 (new). The method according to claim 28, wherein the first criterion is based upon a maximum distance of 1.5 Mb and the second criterion requires a minimum distance of 0.7 Mb.

31 (new). The method according to claim 22, wherein step (ii) of selecting BAC clones is implemented by means of a computer programme.

32 (new). The method according to claim 22, wherein, in step (iii), the BAC clones or the nucleic inserts that they contain, or part of these clones or inserts, are deposited on a support by direct coupling on the support by an interaction with a complementary oligonucleotide, or by means of a spacer arm.

33 (new). The method according to claim 32, wherein the support is level and/or rigid.

34 (new). The method according to claim 32, wherein the support is made with a base of materials chosen from glass, plastic, polymer, metal, biological materials, silicons and nylon.

35 (new). The method according to claim 34, wherein the support is a glass slide.

36 (new). The method according to claim 22, wherein, during step (iii), depositing is implemented according to a pre-specified arrangement and/or density.

37 (new). The method according to claim 22, wherein, prior to step (iii), the clones of the selected set are sub-cultured, amplified, characterised and/or stored.

38 (new). The method for producing a biochip including a support on which has been immobilized a set of polynucleotides, which method comprising the steps of:

(i) obtaining BAC clones including a nucleic insert corresponding to or specific to a portion of a human genome;

(ii) selecting, from the BAC clones thus obtained, a set of BAC clones including a single insert in the human genome, BAC clones of the selected set including nucleic inserts substantially uniformly distributed over the human genome, the selection step comprising:

(a) eliminating non-single clones;

(b) eliminating clones sharing a same STS;

(c) eliminating STS which are marked at at least two different places on the human genome;

(d) classifying clones as a function of their position on the genome to defining neighbouring clones; and

(e) eliminating clones by applying an iterative method so as to obtain in particular substantially uniform distribution of the finally selected clones over the human genome;

(iii) amplifying the BAC clones of the selected set and/or the nucleic inserts that they contain; and

(iv) depositing, on a support, the selected clones or the nucleic inserts contained in said clones, or part of them, under conditions enabling deposited clones or inserts to hybridise with a nucleic acid having a complementary sequence.

39 (new). A biochip that comprises a support on which is immobilized a set of BAC clones including a nucleic insert corresponding to or specific to a portion of a human genome, each clone including a single insert in the human genome and carrying an STS not shared by any other insert of the BAC clones of the set, the BAC clones of the set including nucleic inserts substantially uniformly distributed over the human genome.

40 (new). A method for identifying or locating a nucleic acid on the human genome, comprising placing a nucleic acid in contact with a biochip, in conditions enabling hybridisation between complementary sequences, detection of a hybridisation signal, and identification of the position of the nucleic acid on the genome by identification of the clones involved in the hybridisations, wherein the biochip comprises a support on which is immobilized a set of BAC clones including a nucleic insert corresponding to or specific to a portion of a human genome, each clone including a single insert in the human genome and carrying an STS not shared by any other

insert of the BAC clones of the set, the BAC clones of the set including nucleic inserts substantially uniformly distributed over the human genome.

41 (new). A method for identifying genes associated with a given character trait, comprising (i) identifying fragments of nucleic acids identical between at least two samples taken from subjects having a common character trait, and (ii) hybridising fragments thus identified on a biochip and, (iii) detecting a hybridisation signal, making it possible to locate the fragment(s) on the human genome and thus to identify one or more genes present therein, associated with said character trait, wherein the biochip comprises a support on which is immobilized a set of BAC clones including a nucleic insert corresponding to or specific to a portion of a human genome, each clone including a single insert in the human genome and carrying an STS not shared by any other insert of the BAC clones of the set, the BAC clones of the set including nucleic inserts substantially uniformly distributed over the human genome.